

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: November 5, 2001, 12:58:32 ; Search time 60.22 Seconds  
(without alignments)  
466.762 Million cell updates/sec

Title: US-09-593-316-2  
Perfect score: 2003  
Sequence: 1 MNVKKVILSMILVSTIVIV.....IKLVKMSQTKRYNNRV 369

Scoring table: BLASTOM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1906.5	95.2	368	2	A44785 N-acetylglucosamin
2	1711	85.4	371	2	146583 alpha-1,3-galactos
3	1705.5	85.1	376	2	A56480 N-acetylglucosamin
4	1519	75.8	371	2	146498 alpha-1,3-galactos
5	1471	73.4	394	2	A34417 alpha-1,3-mannosyl
6	673	31.6	295	2	PC1120 fucosylgalactose a
7	671	31.5	343	1	A14933 fucosylgalactose a
8	627	31.3	347	2	JC6126 globoside alpha-N-
9	467	23.3	189	2	PC1168 histo-blood group
10	464.5	23.2	189	2	PC1165 histo-blood group
11	461.5	23.0	189	2	PC1166 histo-blood group
12	459.5	22.9	189	2	PC1173 histo-blood group
13	456.5	22.8	189	2	PC1169 histo-blood group
14	456.5	22.8	189	2	PC1170 histo-blood group
15	456.5	22.8	189	2	PC1171 histo-blood group
16	454.5	22.7	189	2	PC1172 histo-blood group
17	118	5.9	26	2	A39769 N-acetylglucosamin
18	110	5.5	505	2	A32261 aggrase (EC 3.2.1.
19	97.5	4.9	516	1	S44306 phenol 2-monooxyge
20	96	4.8	583	2	S10014 hypothetical prote
21	94.5	4.7	408	2	H64513 hypothetical prote
22	94.5	4.7	563	2	S58198 hypothetical prote
23	94.5	4.7	688	1	TYPTU large T antigen
24	92.5	4.6	390	2	T30395 probable transcrip
25	92	4.6	289	2	B81857 probable acetyltra
26	91.5	4.6	650	2	149523 tumor necrosis fac
27	91.5	4.6	817	2	D86217 protein T27G7.8 (1
28	91	4.5	297	2	F13264 repressor protein
29	91	4.5	788	2	A71076 hypothetical prote

30	90.5	4.5	278	2	F86679 hypothetical prote
31	90.5	4.5	647	2	D75123 probable formate d
32	90	4.5	483	2	T05188 protein kinase F41
33	89.5	4.5	855	2	F71241 probable replicat
34	89.5	4.5	959	2	F72763 probable RNA-dir
35	89.5	4.5	1212	2	144051 hypothetical prote
36	89.5	4.5	1212	2	144051 hypothetical prote
37	89.5	4.5	1212	2	144051 hypothetical prote
38	89	4.4	466	2	T46054 heat shock protein
39	88.5	4.4	517	1	D37831 phenol 2-monooxyge
40	88	4.4	609	2	T14759 hypothetical prote
41	88	4.4	1307	2	H84467 probable reticolem
42	88	4.4	3724	2	T18427 hypothetical prote
43	87	4.3	533	2	T41482 acetylase - f1ss
44	87	4.3	536	1	D08P7 head-to-tail form
45	87	4.3	569	2	A43417 germ cell-less pro

## ALIGNMENTS

RESULT 1  
A44785  
N-acetylglucosamine 3-alpha-galactosyltransferase (EC 2.4.1.124) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1993 #sequence-revision 19-Mar-1993 #text-change 29-Sep-1999  
C:Accession: A44785  
R:Jozlase, D.H.; Shaper, J.H.; Van den Eljnden, D.H.; Van Tuenen, A.J.; Shaper, N.L.  
J. Biol. Chem. 264, 14290-14297, 1989  
A:Title: Bovine alpha1-3-galactosyltransferase: Isolation and characterization of a  
A:Reference number: A44785; MUID:89340543  
A:Accession: A44785  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-368 <J02>  
A:Superfamily: histo-blood group 1 transferase  
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match	95.2%	Score 1906.5;	DB 2;	Length 368;
Best Local Similarity	94.3%	Prod. No. 1;	60-147;	
Matches 348;	Conservative 13;	Mismatches 7;	Indels 1;	Gaps 1;
QY	1	MNVKKVILSMILVSTIVIVVWYIHSPEGSIFWLNPSKNEVSGSSIQKGMFPWFEN	60	
DB	1	MNVKKVILSMILVSTIVIVVWYIHSPEGSIFWLNPSKNEVSGSSIQKGMFPWFEN	59	
QY	61	NGYOEDEDVDHEKQKQKSKLKLSEFNPFFKPEVVTIMKKAIVWGGTYNKAVID	120	
DB	60	NGYHEEDDINEKEQKQKSKLKLSEFNPFFKPEVVTIMKKAIVWGGTYNKAVID	119	
QY	121	DYIAOKITVGLTFAVGRYIEHTLEFLTSANKHEFGHVTIVVWDDVSRMLLELG	180	
DB	120	NYIAOKITVGLTFAVGRYIEHTLEFLTSANKHEFGHVTIVVWDDVSRMLLELG	179	
QY	181	PLRSFKEVFKPKRRQDVSMVRKMTIGEHTVANILOREVDLFCMDVYQVQDPGVETL	240	
DB	180	PLRSFKEVFKPKRRQDVSMVRKMTIGEHTVANILOREVDLFCMDVYQVQDPGVETL	239	
QY	241	GHSVAQDQMWYKADPDEFTTERKESAAVIRPGEGDYTYAAIFGCTPTOVANILQET	300	
DB	240	GHSVAQDQMWYKADPDEFTTERKESAAVIRPGEGDYTYAAIFGCTPTOVANILQET	299	
QY	301	KQILDKKNDIEAOWHDSHLNKKPKILSPYCMQYHIGLPADIKLVKMSQTK	360	
DB	300	KQILDKKNDIEAOWHDSHLNKKPKILSPYCMQYHIGLPADIKLVKMSQTK	359	
QY	361	EYNNVNNV 369		
DB	360	EYNNVNNV 368		



QY	238	ETLSEVAVOIAWNYKAPROFTEYERKEESAAYIPFGSGDYHYAAIFGSPITOVINTQ	297
		:     :     :     :     :     :     :	
Dd	240	ETLSGVAVOIAWNYKASPERFTYERRELSAAYIPFGSGDYHYAAIFGSPITHLNLTR	299
QY	298	ECPFKILEDKRNDIEAWHDESHLNKYFLFNKPRTILSPEYCWYDHIGLPADIKLVKMSW	357
		:     :     :     :     :     :     :     :	
Dd	300	ECFPKILDDKKHDIEAWHDESHLNKYFLFNKPRTIISPPYCMDTQIGLPSDLSKVYAW	359
QY	358	QTKEYNVVRNNV	369
		:	
Dd	360	QTKEYNEVVRNNV	371

RESULT 5  
A34417  
alpha-1,3-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.145)  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-1990 #sequence-revision 15-Jun-1990 #text-change 29-Sep-1999  
C:Accession: A34417  
R:Ratzen, R.D.; Rajan, V.P.; Ruff, M.M.; Kukowska-Latallo, J.; Cummings, R.D.; Lowe, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8227-8231, 1989  
A:Title: Isolation of a cDNA encoding a murine UDPgalactose:beta-D-galactosyl-1,4-N-acetyl-  
A:Reference number: A34417; M01D:90046769  
A:Accession: A34417  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-394 <LAR>  
A:Cross-references: GH:M6925; NID:q193419; P1UD:AAA37657.1; PID:q309242  
C:Superfamily: histo-blood group I transferase  
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match	73.48;	Score 1471;	DB 2;	Length 394;
Best Local Similarity	71.58;	Pred. No. 4.6e-112;		
Matches 266;	Conservative 47;	Mismatches 43;	Indels 16;	Gaps 3

```

QY      1  MNVKGVIILSMIVSVTVVFWMEYHSPEOSLFWINPSRNPEVSGGSSLOKGMWEPMPFN 60
          ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      36  MNVKGVIILMLIVSVTVVFWMEY-----NRIPEY-GENNRQKIDMNEPSPWFK 82

```

Qy 61 NG---YOEDEDVDEKEKQKREKSKLSLSDWENPFKREEVIMTDWAKAPVMEGTYNKA 117  
 11 1111: : 11: : : 11111 11:1:1: 1111:11111: 1  
 Db 83 NGTUSYOEEDNEGRKGRNGR1EEQJLMDWENPKNRDPVLTIVPWKAP1VMEGTYTDA 142

QY 118 VLDVYAKQITVGITFAVGRIIEHYLEEFLSANKHMGHRVI FYVMVDVSRLPLI 177  
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::  
Db 143 LLEYYATQLTGLTFVAVGRIIEHYLEDLFESADMTFMGHRVIFYMIDTSRPVV 202

Gy 178 ELGPIRSKFYEVKPRKRMDVSMVRKMTIGEHIVAHIOREVDLEFCMDVOVFQDFEGV 237  
+ + + : : : : : + : : : : : + : : : : : + : : : : : + : : : : : + : : : : :  
Db 203 HLNPLHSLQVEIRSRKKRWDISMRRKTIGEHLIAHOEVDLFECMDVOVFQDFEGV 262

QY 238 ETLESHVAQLAMWYKADPDEFTYERKRRESAAIIPGEGDFYHIAIFGTPVTYNITQ 297  
|||: ||||||||| : |||||: ||||||||| |||||: |||:  
DB 263 ETLGOLVAGLOAMWKASPHFTYERRLSAAYIPGEDEHYHAIFGTPHTINILTR 322

Dy 298 ECFEGILKDKNDIEQWHDSEHLNKLFFLNKPRTKILSEYCWDTYHIGLPADIKLYKMSW 357

Dp 323 ECFEGTIOGKKHDFPQWHDSEHTNKELFNKPKRTISEYCWDTYHIGLPADIKLYKMSW 382

QY	358	QTKYNNVNNV	369
		:	
DS	383	QTKYNNVNNV	394

## RESULT 6

**EC:2.4.1.40** A2 allele [valid]  
**incosylgalactose alpha-N-acetylalacrosaminyltransferase** (EC 2.4.1.40) A2 allele [valid]  
**incosylgalactose alpha-N-acetylalacrosaminyltransferase** (EC 2.4.1.40) A2 allele [valid]  
**A2 alternate names:** histo-blood group A2 transferase  
**C:Species:** Homo sapiens (man)

C.Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Sep-2000  
C.Accession: PC1120  
K.Yamamoto, F.; McNeill, P.D.; Hakomori, S.

Biochem. Biophys. Res. Commun. 187, 366-374, 1992.  
A:Title: Human histio-blood group A2 transferase coded by A2 allele, one of the A subfamily, the carboxyl terminal.  
A:Reference number: PC1120; MUID:92392351  
A:Accession: PC1120  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-295 <YAN>  
A:Cross-references: cit:544054; NID:q255066; P1DN:AAI23167.1; F1D:q255067  
A:Superfamily: histio-blood group 1 transferase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match	33.68;	Score 673;	DB 2;	Length 295;
Best Local Similarity	46.78;	Pred. No. 2.5e-47;		
Matches 128;	Conservative 49;	Mismatches 95;	Indels 2;	Gaps 2

QY 95 RPEVMTMDWKAPVWEGEYNKRALDDYYAKOKITVGILTVFAVCNRYIHHYLEETLSANK 154  
DB 1 RKDVLVPFWELAPVWEGEENIDLNDEORLONTTIGLVFAIKKYVA-PKLPLETEAK 59

QY 155 HFMGHRVIEFVMWDDVSRLPLIELGPLRSFKVEVKPEBRMQVDSMVRKMTIGEHIVAH 214  
||||||| : | : : : | | : ||||| | : |  
Db 60 HFMGHRRHVHYVFIDQLAARPHVILGTICRQLSVLEVRAYKRWDQDSMRKRMISIDPCTFR 119

Dy 215 IQREVDLFCMDVQVFQDFHFGYETLSGSAOLQAMWYNADPDEFTYERRKNSAAYIPFG 274  
 |||::|||::|:||||: :|||::|:||||:|:||||:  
 Db 120 FLESEVDYLVCADVDMERDRHWAGEILLTEGLTHPCFYGSGRKAATYERRRQSQAATPKD 179

275 EGDFFVYHAAIFGSGTPOVLNTQGFCKILKKKNDIEAMHDESHLNKYPILLNKPTKIL 314  
 180 EGDFFVYLGFGFGSGVOEORLITACHQAMMVDQNGIEAVWHDESHLNKYLILHKKPKVIL 239

QY	335	SPEYCWDRH-IGLPADIKLVKMSWTKEYNVVRN	367
Db	240	SPEYLWDOOLIGMPAVLRLRLFTAVPKNHQAVRN	273

RESULT	7
A34933	

lucosylgalactose alpha-N-acetylglucosaminyltransferase (EC 2.4.99.4) At 40°C, 1%  
 N-1,6-bis(4-methylphenyl)-2,3,5-trimethyl-4-nitrophenyl-beta-D-glucopyranoside  
 N-1,6-bis(4-methylphenyl)-2,3,5-trimethyl-4-nitrophenyl-beta-D-glucopyranoside  
 e; histo-blood group A glycosyltransferase  
 G; species: Homo sapiens (man)

C-Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #extl\_change 08-Sep-2000  
 C-Accession: A34933; S09593; S13173; PC1164  
 R:Yamamoto, F.; Marken, J.; Tsuji, T.; White, T.; Clausen, H.; Hakomori, S.  
 J Biol Chem 265: 1146-1151 1990

A:Title: Cloning and characterization of DNA complementary to human UDP-GalNAc 4-epimerase  
A:Reference number: A34933; MUID:90110098  
A:Accession: A34933

A;Residues: 1-353 <YAM1>  
A;Cross-references: GB:J05175; NID:q340077; PIDN:AAA36792.1; PID:q340078  
R;Yamamoto, F.I.; Clausen, H.; White, T.; Marken, J.; Hakomori, S.I.

A;Title: Molecular genetic basis of the histo-blood group ABO system  
A;Reference number: S09593; MUID:90238543  
A;Accession: S09593

A: Molecule type: mRNA  
A: Residues: 1-353 <1M2>  
R: Navaratnam, N.; Findlay, J. B. C.; Keen, J. N.; Watkins, W. M.

**Artile:** Purification, properties and partial amino acid sequence of the blood group  
**A:** Reference number: S13173; MUID:91024951  
**A:** Accession: S13173

A: Molecular type: protein  
 A: Residues: 'X', 65-73, 'IS', 76-77 <NAV>  
 R: Komlato, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.

A;Title: Animal histo-blood group ABO genes.



Query Match 23.2%: Score 464.5; DB 2; Length 189;

Best Local Similarity 48.7%: Pred. No. 1.3e-30;

Matches 92; Conservative 25; Mismatches 71; Indels 1; Gaps 1;

```

QY 161 RVIFYVWVDVSRMPLIELGRLSKFVFEVKKPERKQDVSVMKKTIGEHIVAHIOREVD 220
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 RVHYVFTDQPAAVPRVTLGTGRLSVLEVRAYKRQDVSMMKMEMISDPCERRFLSEVD 60
QY 221 FLFCMDVDVDFODEGVEITIGESVAQLQAMWKADDEFTYERKRSAAVTPFGGDPFY 280
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 YLVCAVDMEFRDHVGSVEITLPLFGTLHPGFGYSREAFYERKRSQAVIPKDEGDPFY 120
QY 281 HAIFGCTPTQVLTQGEFGKILKDKNDIEAQMWHDESHLNKTYLLNKPTKILSPGYCW 340
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 MGAFFGGSVQVEQRLTRACHQAMWVDQANGIEAVMWHDESHLNKTYLLHKKPTKVLSPGYCW 180
QY 341 DYH-IGLPA 348
  | : | : |
DB 181 DOQLLQMPA 189

```

#### RESULT 11

PC1166

histo-blood group 1 transferrase - chimpanzee (fragment)

N:Alternate names: histo-blood group 2 transferrase

C:Species: Pan troglodytes (chimpanzee)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C:Accession: PC1166; PC1167

R:Komamoto, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.

Biochem. Biophys. Res. Commun. 189, 154-164, 1992

A:Title: Animal histo-blood group ABO genes.

A:Reference number: PC1164; MUID:93080551

A:Accession: PC1166

A:Molecule type: DNA

A:Residues: 1-189 <KOM>

A:Accession: PC1167

A:Molecule type: DNA

A:Residues: 1-189 <KO2>

C:Superfamily: histo-blood group 1 transferrase

Query Match 23.0%: Score 461.5; DB 2; Length 189;

Best Local Similarity 47.6%: Pred. No. 2.3e-30;

Matches 90; Conservative 27; Mismatches 71; Indels 1; Gaps 1;

```

QY 161 RVIFYVWVDVSRMPLIELGRLSKFVFEVKKPERKQDVSVMKKTIGEHIVAHIOREVD 220
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 RVHYVFTDQPAAVPRVTLGTGRLSVLEVRAYKRQDVSMMKMEMISDPCERRFLSEVD 60
QY 221 FLFCMDVDVDFODEGVEITIGESVAQLQAMWKADDEFTYERKRSAAVTPFGGDPFY 280
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 YLVCAVDMEFRDHVGSVEITLPLFGTLHPGFGYSREAFYERKRSQAVIPKDEGDPFY 120
QY 281 HAIFGCTPTQVLTQGEFGKILKDKNDIEAQMWHDESHLNKTYLLNKPTKILSPGYCW 340
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 LGGFFGGSVQVEQRLTRACHQAMWVDQANGIEAVMWHDESHLNKTYLLHKKPTKVLSPGYCW 180
QY 341 DYH-IGLPA 348
  | : | : |
DB 181 DOQLLQMPA 189

```

#### RESULT 12

PC1173

histo-blood group B transferrase - baboon (fragment)

C:Species: Papio sp. (baboon)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C:Accession: PC1173

R:Komamoto, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.

Biochem. Biophys. Res. Commun. 189, 154-164, 1992

A:Title: Animal histo-blood group ABO genes.

A:Reference number: PC1164; MUID:93080551

A:Accession: PC1173

A:Molecule type: DNA

A:Residues: 1-189 <KOM>

C:Superfamily: histo-blood group 1 transferrase

Query Match 22.9%: Score 459.5; DB 2; Length 189;

Best Local Similarity 48.1%: Pred. No. 3.3e-30;

Matches 91; Conservative 25; Mismatches 72; Indels 1; Gaps 1;

```

QY 161 RVIFYVWVDVSRMPLIELGRLSKFVFEVKKPERKQDVSVMKKTIGEHIVAHIOREVD 220
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 RVHYVFTDQPAAVPRVTLGTGRLSVLEVRAYKRQDVSMMKMEMISDPCERRFLSEVD 60
QY 221 FLFCMDVDVDFODEGVEITIGESVAQLQAMWKADDEFTYERKRSAAVTPFGGDPFY 280
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 YLVCAVDMEFRDHVGSVEITLPLFGTLHPGFGYSREAFYERKRSQAVIPKDEGDPFY 120
QY 281 HAIFGCTPTQVLTQGEFGKILKDKNDIEAQMWHDESHLNKTYLLNKPTKILSPGYCW 340
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 MGAFFGGSVQVEQRLTRACHQAMWVDQANGIEAVMWHDESHLNKTYLLHKKPTKVLSPGYCW 180
QY 341 DYH-IGLPA 348
  | : | : |
DB 181 DOQLLQMPA 189

```

#### RESULT 13

PC1169

histo-blood group 1 transferrase - orangutan (fragment)

C:Species: Pongo pygmaeus (orangutan)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C:Accession: PC1169

R:Komamoto, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.

Biochem. Biophys. Res. Commun. 189, 154-164, 1992

A:Title: Animal histo-blood group ABO genes.

A:Reference number: PC1164; MUID:93080551

A:Accession: PC1169

A:Molecule type: DNA

A:Residues: 1-189 <KOM>

C:Superfamily: histo-blood group 1 transferrase

Query Match 22.8%: Score 456.5; DB 2; Length 189;

Best Local Similarity 47.6%: Pred. No. 5.8e-30;

Matches 90; Conservative 26; Mismatches 72; Indels 1; Gaps 1;

```

QY 161 RVIFYVWVDVSRMPLIELGRLSKFVFEVKKPERKQDVSVMKKTIGEHIVAHIOREVD 220
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 RVHYVFTDQPAAVPRVTLGTGRLSVLEVRAYKRQDVSMMKMEMISDPCERRFLSEVD 60
QY 221 FLFCMDVDVDFODEGVEITIGESVAQLQAMWKADDEFTYERKRSAAVTPFGGDPFY 280
  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 YLVCAVDMEFRDHVGSVEITLPLFGTLHPGFGYSREAFYERKRSQAVIPKDEGDPFY 120
QY 281 HAIFGCTPTQVLTQGEFGKILKDKNDIEAQMWHDESHLNKTYLLNKPTKILSPGYCW 340
  ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 LGGFFGGSVQVEQRLTRACHQAMWVDQANGIEAVMWHDESHLNKTYLLHKKPTKVLSPGYCW 180
QY 341 DYH-IGLPA 348
  | : | : |
DB 181 DOQLLQMPA 189

```

#### RESULT 14

PC1170

histo-blood group 2 transferrase - orangutan (fragment)

C:Species: Pongo pygmaeus (orangutan)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 07-May-1999

C:Accession: PC1170

R:Komamoto, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.

Biochem. Biophys. Res. Commun. 189, 154-164, 1992

A:Title: Animal histo-blood group ABO genes.

